<110> Kossida, Sophia

<120> Regulation of Ceramide Kinase

<130> 004974.00951

<150> US 09/969,896
<151> 2001-10-04

<150> US 60/238,005
<151> 2000-10-06

<150> US 60/314,113
<151> 2001-08-23

<160> 16

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 979
<212> DNA
<213> Homo sapiens

<400> 1
```
accaaagcat ttactggtat ttatcaaccc gtttggagga aaaggacaag gcaagcggat      60
atatgaaaga aaagtggcac cactgttcac cttagcctcc atcaccactg acatcatcgg     120
taacaaattc tatgttaact atgtagaagt aattactgaa catgctaatc aggccaagga     180
gactctgtat gagattaaca tagacaaata cgacggcatc gtctgtgtcg gcggagatgg     240
tatgttcagc gaggtgctgc acggtctgat tgggaggacg cagaggagcg ccggggtcga     300
ccagaaccac ccccgggctg tgctggtccc cagtagcctc cggattggaa tcattcccgc     360
agggtcaacg gactgcgtgt gttactccac cgtgggcacc agcgacgcag aaacctcggc     420
gctgcatatc gttgttgggg actcgctggc catggatgtg tcctcagtcc accacaacag     480
cacactcctt cgctactccg tgtccctgct gggctacggc ttctacgggg acatcatcaa     540
ggacagtgag aagaaacggt ggttgggtct tgccagatac gacttttcag gtttaaagac     600
cttcctctcc caccactgct atgaagggac agtgtccttc ctccctgcac aacacacggt     660
gggatctcca agggatagga agccctgccg ggcaggatgc tttgtttgca ggcaaagcaa     720
gcagcagctg gaggaggagc agaagaaagc actgtatggt ttggaagctg cggaggacgt     780
ggaggagtgg caagtcgtct gtgggaagtt tctggccatc aatgccacaa acatgtcctg     840
tgcttgtcgc cggagcccca ggggcctctc cccggctgcc cacttgggag acgggtcttc     900
tgacctcatc ctcatccgga aatgctccag gttcaatttt ctgagatttc tcatcaggca     960
caccaaccag caggaccag                                                  979
```

<210> 2
<211> 326
<212> PRT
<213> Homo sapiens

<400> 2

```
Pro Lys His Leu Leu Val Phe Ile Asn Pro Phe Gly Gly Lys Gly Gln
 1               5                  10                  15
Gly Lys Arg Ile Tyr Glu Arg Lys Val Ala Pro Leu Phe Thr Leu Ala
            20              25                  30
Ser Ile Thr Thr Asp Ile Ile Gly Asn Lys Phe Tyr Val Asn Tyr Val
        35                  40                  45
Glu Val Ile Thr Glu His Ala Asn Gln Ala Lys Glu Thr Leu Tyr Glu
    50                  55                  60
Ile Asn Ile Asp Lys Tyr Asp Gly Ile Val Cys Val Gly Gly Asp Gly
65                  70                  75                  80
Met Phe Ser Glu Val Leu His Gly Leu Ile Gly Arg Thr Gln Arg Ser
            85                  90                  95
Ala Gly Val Asp Gln Asn His Pro Arg Ala Val Leu Val Pro Ser Ser
            100                 105                 110
Leu Arg Ile Gly Ile Ile Pro Ala Gly Ser Thr Asp Cys Val Cys Tyr
        115                 120                 125
Ser Thr Val Gly Thr Ser Asp Ala Glu Thr Ser Ala Leu His Ile Val
        130                 135                 140
Val Gly Asp Ser Leu Ala Met Asp Val Ser Ser Val His His Asn Ser
145                 150                 155                 160
Thr Leu Leu Arg Tyr Ser Val Ser Leu Leu Gly Tyr Gly Phe Tyr Gly
                165                 170                 175
Asp Ile Ile Lys Asp Ser Glu Lys Lys Arg Trp Leu Gly Leu Ala Arg
            180                 185                 190
Tyr Asp Phe Ser Gly Leu Lys Thr Phe Leu Ser His His Cys Tyr Glu
            195                 200                 205
Gly Thr Val Ser Phe Leu Pro Ala Gln His Thr Val Gly Ser Pro Arg
    210                 215                 220
Asp Arg Lys Pro Cys Arg Ala Gly Cys Phe Val Cys Arg Gln Ser Lys
225                 230                 235                 240
Gln Gln Leu Glu Glu Glu Gln Lys Lys Ala Leu Tyr Gly Leu Glu Ala
            245                 250                 255
Ala Glu Asp Val Glu Glu Trp Gln Val Val Cys Gly Lys Phe Leu Ala
            260                 265                 270
Ile Asn Ala Thr Asn Met Ser Cys Ala Cys Arg Arg Ser Pro Arg Gly
        275                 280                 285
Leu Ser Pro Ala Ala His Leu Gly Asp Gly Ser Ser Asp Leu Ile Leu
    290                 295                 300
Ile Arg Lys Cys Ser Arg Phe Asn Phe Leu Arg Phe Leu Ile Arg His
305                 310                 315                 320
Thr Asn Gln Gln Asp Gln
                325
```

<210> 3
<211> 638
<212> PRT
<213> Homo sapiens

<400> 3

```
Met Ala Pro Pro Pro Pro Leu Ala Ala Ser Thr Pro Leu Leu His
 1           5                  10              15
Gly Glu Phe Gly Ser Tyr Pro Ala Arg Gly Pro Arg Phe Ala Leu Thr
            20              25              30
Leu Thr Ser Gln Ala Leu His Ile Gln Arg Leu Arg Pro Phe Thr Lys
        35              40              45
Pro Glu Ala Arg Pro Arg Gly Gly Leu Val Pro Leu Ala Glu Val Ser
    50              55              60
Gly Cys Cys Thr Leu Arg Ser Arg Ser Pro Ser Asp Ser Ala Ala Tyr
65              70              75              80
Phe Cys Ile Tyr Thr Tyr Pro Arg Gly Arg Arg Gly Ala Arg Arg Arg
            85              90              95
Ala Thr Arg Thr Phe Arg Ala Asp Gly Ala Phe Thr Ala Thr Tyr Glu
        100             105             110
Glu Asn Arg Ala Glu Ala Gln Arg Trp Ala Thr Ala Leu Thr Cys Leu
        115             120             125
Leu Arg Gly Leu Pro Leu Pro Gly Asp Gly Glu Ile Thr Pro Asp Leu
    130             135             140
Leu Pro Arg Pro Pro Arg Leu Leu Leu Leu Val Asn Pro Phe Gly Gly
145             150             155             160
Arg Gly Leu Ala Trp Gln Trp Phe Thr Cys Lys Asn His Val Leu Pro
            165             170             175
Met Ile Ser Glu Ala Gly Leu Ser Phe Asn Leu Ile Gln Thr Glu Arg
            180             185             190
Gln Asn His Ala Arg Glu Leu Val Gln Gly Leu Ser Leu Ser Glu Trp
        195             200             205
Asp Gly Ile Val Thr Val Ser Gly Asp Gly Leu Leu His Glu Val Leu
    210             215             220
Asn Gly Leu Leu Phe Thr Asp Arg Pro Asp Trp Glu Glu Ala Val Lys
225             230             235             240
Met Pro Val Gly Ile Leu Pro Cys Gly Ser Gly Asn Ala Leu Ala Gly
            245             250             255
Ala Val Asn Gln His Gly Gly Phe Glu Pro Ala Leu Gly Leu Asp Leu
        260             265             270
Leu Leu Asn Cys Ser Leu Leu Leu Cys Arg Gly Gly Gly His Pro Leu
        275             280             285
Asp Phe Thr Leu Leu Ser Val Thr Leu Ala Ser Gly Ser Arg Cys Phe
    290             295             300
Ser Phe Leu Ser Val Ala Trp Gly Phe Val Ser Asp Val Asp Ile Gln
305             310             315             320
Ser Glu Arg Phe Arg Ala Leu Gly Ser Ala Arg Phe Thr Leu Gly Thr
            325             330             335
Val Leu Gly Leu Ala Thr Leu His Thr Tyr Arg Gly Arg Leu Phe Thr
            340             345             350
Ser Tyr Leu Pro Ala Thr Val Glu Pro Ala Ser Pro Thr Pro Ala His
        355             360             365
Ser Leu Pro Arg Ala Lys Ser Glu Leu Thr Leu Thr Pro Asp Pro Ala
    370             375             380
Pro Pro Met Ala His Ser Pro Leu His Arg Ser Val Ser Asp Leu Pro
385             390             395             400
```

- 3 -

```
Leu Pro Leu Pro Gln Pro Ala Leu Ala Ser Pro Phe Thr Gly Ser Pro
            405                 410                 415
Glu Pro Leu Pro Ile Leu Ser Leu Asn Gly Gly Gly Pro Glu Leu Ala
            420                 425                 430
Gly Asp Trp Gly Gly Ala Gly Asp Ala Pro Leu Ser Pro Asp Pro Leu
            435                 440                 445
Leu Ser Ser Pro Pro Gly Ser Pro Lys Ala Ala Leu His Ser Pro Val
        450                 455                 460
Ser Glu Gly Ala Pro Val Ile Pro Phe Thr Pro Ser Ser Gly Leu Pro
465                 470                 475                 480
Leu Pro Thr Pro Asp Ala Arg Val Gly Ala Ser Thr Cys Gly Pro Pro
                485                 490                 495
Asp His Leu Leu Pro Pro Leu Gly Thr Pro Leu Pro Pro Asp Trp Val
            500                 505                 510
Thr Leu Glu Gly Asp Phe Val Leu Met Leu Ala Ile Ser Pro Ser His
            515                 520                 525
Leu Gly Ala Asp Leu Phe Thr Val Ala Ala Pro His Ala Arg Phe Asp
        530                 535                 540
Asp Gly Leu Val His Leu Cys Trp Val Arg Ser Gly Ile Ser Arg Ala
545                 550                 555                 560
Ala Leu Leu Arg Leu Phe Leu Ala Met Glu Arg Gly Ser His Phe Ser
                565                 570                 575
Leu Gly Cys Pro Gln Leu Gly Tyr Ala Ala Ala Arg Ala Phe Arg Leu
                580                 585                 590
Glu Pro Phe Thr Leu Thr Pro Arg Gly Val Leu Thr Val Asp Gly Glu
            595                 600                 605
Gln Val Glu Tyr Gly Pro Leu Gln Ala Gln Met His Pro Gly Ile Gly
        610                 615                 620
Thr Leu Leu Thr Gly Pro Pro Gly Cys Pro Gly Arg Glu Pro
625                 630                 635

<210> 4
<211> 474
<212> DNA
<213> Homo sapiens

<400> 4
cacgaggggt atgttcagcg aggtgctgca cggtctgatt gggaggacgc agaggagcgc        60
cggggtcgac cagaaccacc cccgggctgt gctggtcccc agtagcctcc ggattggaat       120
cattcccgca gggtcaacgg actgcgtgtg ttactccacc gtgggcacca gcgacgcaga       180
aacctcggcg ctgcatatcg ttgttgggga ctcgctggcc atggatgtgt cctcagtcca       240
ccacaacagc acactccttc gctactccgt gtccctgctg ggctacggct tctacgggga       300
catcatcaag gacagtgaga agaaacggtg gttgggtctt gccagatacg acttttcagg       360
tttaaagacc ttcctctccc accactgcta tgaagggaca gtgtccttcc tccctgcaca       420
acacacggtg ggatctccaa gggataggaa gccctgccgg gcaagatgct ttgg            474

<210> 5
<211> 329
<212> DNA
<213> Homo sapiens
```

<220>
<221> misc_feature
<222> (1)...(329)
<223> n = A,T,C or G

<400> 5
tcaccactga catcatcgtt actgaacatg ctantcaggc canggagact ctgtatgaga   60
ttaacataga caaatacgac ggcatcgtct gtgtcggcgg agatggtatg ttcagcgagg   120
tgctgcacgg tctgattggg aggacgcaga ggagcgccgg ggtcgaccag aaccaccccc   180
gggctgtgct ggtccccagt agcctccgga ttggaatcat tcccgcaggt caaacggact   240
gcgtgtntta ctccaccgtg ggcancagcg acgcagaaac ctcggcgctg catatcgttg   300
ttggggactc gctggccatg gatgtgtcc   329

<210> 6
<211> 167
<212> DNA
<213> Homo sapiens

<400> 6
gtttaaagac cttcctctcc caccactgct atgaagggac agtgtccttc ctccctgcac   60
aacacacggt gggatctcca agggatagga agccctgccg ggcaggatgc tttgtttgca   120
ggcaaagcaa gcagcagctg gaggaggagc agaagaaagc actgtat   167

<210> 7
<211> 153
<212> DNA
<213> Homo sapiens

<400> 7
gggactcgct ggccatggat gtgtcctcag tccaccacaa cagcacactc cttcgctact   60
ccgtgtccct gctgggctac ggcttctacg gggacatcat caaggacagt gagaagaaac   120
ggtggttggg tcttgccaga tacgactttt cag   153

<210> 8
<211> 550
<212> DNA
<213> Homo sapiens

<400> 8
cacgaggccg ctaacggtcc ggcgcccctc ggcgtccgcg cgcccccagc ctggcggacg   60
agcccggcgg cggagatggg ggcgacgggg gcggcggagc cgctgcaatc cgtgctgtgg   120
gtgaagcagc agcgctgcgc cgtgagcctg gagcccgcgc gggctctgct gcgctggtgg   180
cggagcccgg ggcccggagc cggcgcccccc ggcgcggatg cctgctctgt gcctgtatct   240
gagatcatcg ccgttgagga aacagacgtt cacgggaaac atcaaggcag tggaaaatgg   300
cagaaaatgg aaaagcctta cgcttttaca gttcactgtg taaagagagc acgacggcac   360
cgctggaagt gggcgcaggt gactttctgg tgtccagagg agcagctgtg tcacttgtgg   420
ctgcagaccc tgcgggagat gctggagaag ctgacgtcca gaccaaagca tttactggta   480
tttatcaacc cgtttggagg aaaaggacaa ggcaagcgga tatatgaaag aaaagtggca   540
ccactgttca   550

<210> 9
<211> 1614
<212> DNA
<213> Homo sapiens

<400> 9
atggggggcga cggggggcggc ggagccgctg caatccgtgc tgtgggtgaa gcagcagcgc   60
tgcgccgtga gcctggagcc cgcgcggggct ctgctgcgct ggtggcggag cccggggccc   120
ggagccggcg cccccggcgc ggatgcctgc tctgtgcctg tatctgagat catcgccgtt   180
gaggaaacag acgttcacgg gaaacatcaa ggcagtggaa aatggcagaa aatggaaaag   240
ccttacgctt ttacagttca ctgtgtaaag agagcacgac ggcaccgctg gaagtgggcg   300
caggtgactt tctggtgtcc agaggagcag ctgtgtcact tgtggctgca gaccctgcgg   360
gagatgctgg agaagctgac gtccagacca aagcatttac tggtatttat caacccgttt   420
ggaggaaaag acaaggcaa gcggatatat gaaagaaaag tggcaccact gttcacctta   480
gcctccatca ccactgacat catcgttact gaacatgcta atcaggccaa ggagactctg   540
tatgagatta acatagacaa atacgacggc atcgtctgtg tcggcggaga tggtatgttc   600
agcgaggtgc tgcacggtct gattgggagg acgcagagga gcgccggggt cgaccagaac   660
cacccccggg ctgtgctggt ccccagtagc ctccggattg gaatcattcc cgcagggtca   720
acggactgcg tgtgttactc caccgtgggc accagcgacg cagaaacctc ggcgctgcat   780
atcgttgttg gggactcgct ggccatggat gtgtcctcag tccaccacaa cagcacactc   840
cttcgctact ccgtgtccct gctgggctac ggcttctacg gggacatcat caaggacagt   900
gagaagaaac ggtggttggg tcttgccaga tacgactttt caggtttaaa gaccttcctc   960
tcccaccact gctatgaagg gacagtgtcc ttcctccctg cacaacacac ggtgggatct   1020
ccaagggata ggaagccctg ccgggcagga tgctttgttt gcaggcaaag caagcagcag   1080
ctggaggagg agcagaagaa agcactgtat ggtttggaag ctgcggagga cgtggaggag   1140
tggcaagtcg tctgtgggaa gtttctggcc atcaatgcca caaacatgtc ctgtgcttgt   1200
cgccggagcc ccaggggcct ctccccggct gcccacttgg gagacgggtc ttctgacctc   1260
atcctcatcc ggaaatgctc caggttcaat tttctgagat ttctcatcag gcacaccaac   1320
cagcaggacc agtttgactt cactttttgtt gaagtttatc gcgtcaagaa attccagttt   1380
acgtcgaagc acatggagga tgaggacagc gacctcaagg agggggggaa gaagcgcttt   1440
gggcacattt gcagcagcca cccctcctgc tgctgcaccg tctccaacag ctcctggaac   1500
tgcgacgggg aggtcctgca cagccctgcc atcgaggtca gagtccactg ccagctggtt   1560
cgactctttg cacgaggaat tgaagagaat ccgaagccag actcacacag ctga   1614

<210> 10
<211> 537
<212> PRT
<213> Homo sapiens

<400> 10
Met Gly Ala Thr Gly Ala Ala Glu Pro Leu Gln Ser Val Leu Trp Val
1   5   10   15
Lys Gln Gln Arg Cys Ala Val Ser Leu Glu Pro Ala Arg Ala Leu Leu
            20   25   30
Arg Trp Trp Arg Ser Pro Gly Pro Gly Ala Gly Ala Pro Gly Ala Asp
            35   40   45
Ala Cys Ser Val Pro Val Ser Glu Ile Ile Ala Val Glu Glu Thr Asp
        50   55   60
Val His Gly Lys His Gln Gly Ser Gly Lys Trp Gln Lys Met Glu Lys

-6-

```
      65                    70                    75                    80
Pro Tyr Ala Phe Thr Val His Cys Val Lys Arg Ala Arg Arg His Arg
              85                    90                    95
Trp Lys Trp Ala Gln Val Thr Phe Trp Cys Pro Glu Glu Gln Leu Cys
             100                   105                   110
His Leu Trp Leu Gln Thr Leu Arg Glu Met Leu Glu Lys Leu Thr Ser
             115                   120                   125
Arg Pro Lys His Leu Leu Val Phe Ile Asn Pro Phe Gly Gly Lys Gly
         130                   135                   140
Gln Gly Lys Arg Ile Tyr Glu Arg Lys Val Ala Pro Leu Phe Thr Leu
145                   150                   155                   160
Ala Ser Ile Thr Thr Asp Ile Ile Val Thr Glu His Ala Asn Gln Ala
             165                   170                   175
Lys Glu Thr Leu Tyr Glu Ile Asn Ile Asp Lys Tyr Asp Gly Ile Val
             180                   185                   190
Cys Val Gly Gly Asp Gly Met Phe Ser Glu Val Leu His Gly Leu Ile
             195                   200                   205
Gly Arg Thr Gln Arg Ser Ala Gly Val Asp Gln Asn His Pro Arg Ala
         210                   215                   220
Val Leu Val Pro Ser Ser Leu Arg Ile Gly Ile Ile Pro Ala Gly Ser
225                   230                   235                   240
Thr Asp Cys Val Cys Tyr Ser Thr Val Gly Thr Ser Asp Ala Glu Thr
             245                   250                   255
Ser Ala Leu His Ile Val Val Gly Asp Ser Leu Ala Met Asp Val Ser
             260                   265                   270
Ser Val His His Asn Ser Thr Leu Leu Arg Tyr Ser Val Ser Leu Leu
             275                   280                   285
Gly Tyr Gly Phe Tyr Gly Asp Ile Ile Lys Asp Ser Glu Lys Lys Arg
         290                   295                   300
Trp Leu Gly Leu Ala Arg Tyr Asp Phe Ser Gly Leu Lys Thr Phe Leu
305                   310                   315                   320
Ser His His Cys Tyr Glu Gly Thr Val Ser Phe Leu Pro Ala Gln His
             325                   330                   335
Thr Val Gly Ser Pro Arg Asp Arg Lys Pro Cys Arg Ala Gly Cys Phe
             340                   345                   350
Val Cys Arg Gln Ser Lys Gln Gln Leu Glu Glu Glu Gln Lys Lys Ala
             355                   360                   365
Leu Tyr Gly Leu Glu Ala Ala Glu Asp Val Glu Glu Trp Gln Val Val
             370                   375                   380
Cys Gly Lys Phe Leu Ala Ile Asn Ala Thr Asn Met Ser Cys Ala Cys
385                   390                   395                   400
Arg Arg Ser Pro Arg Gly Leu Ser Pro Ala Ala His Leu Gly Asp Gly
             405                   410                   415
Ser Ser Asp Leu Ile Leu Ile Arg Lys Cys Ser Arg Phe Asn Phe Leu
             420                   425                   430
Arg Phe Leu Ile Arg His Thr Asn Gln Gln Asp Gln Phe Asp Phe Thr
             435                   440                   445
Phe Val Glu Val Tyr Arg Val Lys Lys Phe Gln Phe Thr Ser Lys His
             450                   455                   460
Met Glu Asp Glu Asp Ser Asp Leu Lys Glu Gly Gly Lys Lys Arg Phe
```

-7-

```
465                     470                     475                     480
Gly His Ile Cys Ser Ser His Pro Ser Cys Cys Cys Thr Val Ser Asn
                485                     490                     495
Ser Ser Trp Asn Cys Asp Gly Glu Val Leu His Ser Pro Ala Ile Glu
            500                     505                     510
Val Arg Val His Cys Gln Leu Val Arg Leu Phe Ala Arg Gly Ile Glu
        515                     520                     525
Glu Asn Pro Lys Pro Asp Ser His Ser
        530                     535


<210> 11
<211> 562
<212> PRT
<213> Homo sapiens


<400> 11
His Glu Ala Ala Asn Gly Pro Ala Pro Leu Gly Val Arg Ala Pro Pro
 1               5                   10                  15
Ala Trp Arg Thr Ser Pro Ala Ala Glu Met Gly Ala Thr Gly Ala Ala
            20                  25                  30
Glu Pro Leu Gln Ser Val Leu Trp Val Lys Gln Gln Arg Cys Ala Val
        35                  40                  45
Ser Leu Glu Pro Ala Arg Ala Leu Leu Arg Trp Trp Arg Ser Pro Gly
    50                  55                  60
Pro Gly Ala Gly Ala Pro Gly Ala Asp Ala Cys Ser Val Pro Val Ser
65                  70                  75                  80
Glu Ile Ile Ala Val Glu Glu Thr Asp Val His Gly Lys His Gln Gly
                85                  90                  95
Ser Gly Lys Trp Gln Lys Met Glu Lys Pro Tyr Ala Phe Thr Val His
            100                 105                 110
Cys Val Lys Arg Ala Arg Arg His Arg Trp Lys Trp Ala Gln Val Thr
            115                 120                 125
Phe Trp Cys Pro Glu Glu Gln Leu Cys His Leu Trp Leu Gln Thr Leu
    130                 135                 140
Arg Glu Met Leu Glu Lys Leu Thr Ser Arg Pro Lys His Leu Leu Val
145                 150                 155                 160
Phe Ile Asn Pro Phe Gly Gly Lys Gly Gln Gly Lys Arg Ile Tyr Glu
                165                 170                 175
Arg Lys Val Ala Pro Leu Phe Thr Leu Ala Ser Ile Thr Thr Asp Ile
            180                 185                 190
Ile Val Thr Glu His Ala Asn Gln Ala Lys Glu Thr Leu Tyr Glu Ile
        195                 200                 205
Asn Ile Asp Lys Tyr Asp Gly Ile Val Cys Val Gly Gly Asp Gly Met
    210                 215                 220
Phe Ser Glu Val Leu His Gly Leu Ile Gly Arg Thr Gln Arg Ser Ala
225                 230                 235                 240
Gly Val Asp Gln Asn His Pro Arg Ala Val Leu Val Pro Ser Ser Leu
            245                 250                 255
Arg Ile Gly Ile Ile Pro Ala Gly Ser Thr Asp Cys Val Cys Tyr Ser
            260                 265                 270
```

```
Thr Val Gly Thr Ser Asp Ala Glu Thr Ser Ala Leu His Ile Val Val
        275                 280                 285
Gly Asp Ser Leu Ala Met Asp Val Ser Ser Val His His Asn Ser Thr
    290                 295                 300
Leu Leu Arg Tyr Ser Val Ser Leu Leu Gly Tyr Gly Phe Tyr Gly Asp
305                 310                 315                 320
Ile Ile Lys Asp Ser Glu Lys Lys Arg Trp Leu Gly Leu Ala Arg Tyr
                325                 330                 335
Asp Phe Ser Gly Leu Lys Thr Phe Leu Ser His His Cys Tyr Glu Gly
            340                 345                 350
Thr Val Ser Phe Leu Pro Ala Gln His Thr Val Gly Ser Pro Arg Asp
        355                 360                 365
Arg Lys Pro Cys Arg Ala Gly Cys Phe Val Cys Arg Gln Ser Lys Gln
    370                 375                 380
Gln Leu Glu Glu Glu Gln Lys Lys Ala Leu Tyr Gly Leu Glu Ala Ala
385                 390                 395                 400
Glu Asp Val Glu Glu Trp Gln Val Val Cys Gly Lys Phe Leu Ala Ile
                405                 410                 415
Asn Ala Thr Asn Met Ser Cys Ala Cys Arg Arg Ser Pro Arg Gly Leu
            420                 425                 430
Ser Pro Ala Ala His Leu Gly Asp Gly Ser Ser Asp Leu Ile Leu Ile
        435                 440                 445
Arg Lys Cys Ser Arg Phe Asn Phe Leu Arg Phe Leu Ile Arg His Thr
    450                 455                 460
Asn Gln Gln Asp Gln Phe Asp Phe Thr Phe Val Glu Val Tyr Arg Val
465                 470                 475                 480
Lys Lys Phe Gln Phe Thr Ser Lys His Met Glu Asp Glu Asp Ser Asp
            485                 490                 495
Leu Lys Glu Gly Gly Lys Lys Arg Phe Gly His Ile Cys Ser Ser His
            500                 505                 510
Pro Ser Cys Cys Cys Thr Val Ser Asn Ser Ser Trp Asn Cys Asp Gly
            515                 520                 525
Glu Val Leu His Ser Pro Ala Ile Glu Val Arg Val His Cys Gln Leu
    530                 535                 540
Val Arg Leu Phe Ala Arg Gly Ile Glu Glu Asn Pro Lys Pro Asp Ser
545                 550                 555                 560
His Ser
```

<210> 12
<211> 24
<212> DNA
<213> Homo sapiens

<400> 12
cgctgcatat cgttgttggg gact   24

<210> 13
<211> 24
<212> DNA

<213> Homo sapiens

<220>
<223> random oligonucleotide

<400> 13
cgctgcatat cgttgttggg gact   24

<210> 14
<211> 24
<212> DNA
<213> Homo sapiens

<400> 14
tggtttcgta aatgaccata aata   24

<210> 15
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> random oligonucleotide

<400> 15
tcaactgact agatgtacat ggac   24

<210> 16
<211> 4413
<212> DNA
<213> Homo sapiens

<400> 16
cacgaggccg ctaacggtcc ggcgcccctc ggcgtccgcg cgcccccagc ctggcggacg   60
agcccggcgg cggagatggg ggcgacgggg gcggcggagc cgctgcaatc cgtgctgtgg   120
gtgaagcagc agcgctgcgc cgtgagcctg gagcccgcgc gggctctgct gcgctggtgg   180
cggagcccgg ggcccggagc cggcgccccc ggcgcggatg cctgctctgt gcctgtatct   240
gagatcatcg ccgttgagga aacagacgtt cacgggaaac atcaaggcag tggaaaatgg   300
cagaaaatgg aaaagcctta cgcttttaca gttcactgtg taaagagagc acgacggcac   360
cgctggaagt gggcgcaggt gactttctgg tgtccagagg agcagctgtg tcacttgtgg   420
ctgcagaccc tgcgggagat gctggagaag ctgacgtcca gaccaaagca tttactggta   480
tttatcaacc cgtttggagg aaaaggacaa ggcaagcgga tatatgaaag aaaagtggca   540
ccactgttca ccttagcctc catcaccact gacatcatcg ttactgaaca tgctaatcag   600
gccaaggaga ctctgtatga gattaacata gacaaatacg acggcatcgt ctgtgtcggc   660
ggagatggta tgttcagcga ggtgctgcac ggtctgattg ggaggacgca gaggagcgcc   720
ggggtcgacc agaaccaccc ccgggctgtg ctggtcccca gtagcctccg gattggaatc   780
attcccgcag ggtcaacgga ctgcgtgtgt tactccaccg tgggcaccag cgacgcagaa   840
acctcggcgc tgcatatcgt tgttggggac tcgctggcca tggatgtgtc ctcagtccac   900
cacaacagca cactccttcg ctactccgtg tccctgctgg gctacggctt ctacggggac   960
atcatcaagg acagtgagaa gaaacggtgg ttgggtcttg ccagatacga cttttcaggt   1020

004974.00951
LBRI-221/LIO-160

- 10 -

```
ttaaagacct tcctctccca ccactgctat gaagggacag tgtccttcct ccctgcacaa      1080
cacacggtgg gatctccaag ggataggaag ccctgccggg caggatgctt tgtttgcagg      1140
caaagcaagc agcagctgga ggaggagcag aagaaagcac tgtatggttt ggaagctgcg      1200
gaggacgtgg aggagtggca agtcgtctgt gggaagtttc tggccatcaa tgccacaaac      1260
atgtcctgtg cttgtcgccg gagccccagg ggcctctccc cggctgccca cttgggagac      1320
gggtcttctg acctcatcct catccggaaa tgctccaggt tcaattttct gagatttctc      1380
atcaggcaca ccaaccagca ggaccagttt gacttcactt ttgttgaagt ttatcgcgtc      1440
aagaaattcc agtttacgtc gaagcacatg gaggatgagg acagcgacct caaggagggg      1500
gggaagaagc gctttgggca catttgcagc agccacccct cctgctgctg caccgtctcc      1560
aacagctcct ggaactgcga cggggaggtc ctgcacagcc ctgccatcga ggtcagagtc      1620
cactgccagc tggttcgact ctttgcacga ggaattgaag agaatccgaa gccagactca      1680
cacagctgag aagccggcgt cctgctctcg aactgggaaa gtgtgaaaac tatttaagat      1740
aattattaca gaccaattat gttgatatat acatttaaat gtagaaattt atttttgata      1800
gttaaatctt gattttagaa gaaaaccctt ttgtcaacaa ttttgtgtac atatttggca      1860
ttttcagttc tgtacgcatc tgcggggttgc agcccacgcc gcttactctc agcggatgca      1920
gctgctcact tgggggcact ggcctcttag gttttaacga tgtcaacagt gtagtttaga      1980
aaatggcccg ttagtggctc tattgcaata atgttaggga cattatatga tttccacgca      2040
ggtcacacca tctgggcctg aggtagcagt gggtcacttt gatccacttt gcaggactta      2100
ttctgtaacg gtttgtggcc aagttttggg aagtggttga ttctctttgc cttcatttca      2160
ccttcctctt cgtttacggt taggacatcg ctgcttgatc cttacaatac tgtgcaactg      2220
caatgcaacg tggccctgct tcaggtgatc cgcgggaggg gcctccacgc cagcgccggg      2280
aaggctgctg gggcctccac acctgcctca tcacggcggc gaggctacga caatccggct      2340
gggagcatga ccttggcgtc tgttctggga gcacagatga taagctctgg aagctggcag      2400
tgtgtaaagc actggcaagt ttgttactgt taaaatgtca aataccaatg ctttatatcg      2460
acgcgaagtg cttaacacag ccgggcttgg gggcagtcag gaggaagctg gccatccgtg      2520
gaggaggggc cggtcctgga ctcccgcagg actcctctga tgcagggcct gaagtctgta      2580
cacgtggtcc agatttgtcc ttgtcttttc ttcacactga gttctctata tttattgaac      2640
atcttgtcct tttaagccag agtagtgtaa actgcgtctc ggatgtctgt cttttgcctc      2700
gaagccacga tggatcgctg gtttcctctg cagcgcgagg gctccggcga ccagaggatt      2760
cttcccggaa ggcattcctg ccgcgctccc cggggcaccc ctcaattgtg tactacgtcc      2820
ttgtttagtg tgtatccgtg cccacgtaga tgatgtctgt aacgtagttt tgtttgaaat      2880
atgagaatat gcggcttaaa ctttgatctg taaggagcgg ggccgtggcc gtttggagca      2940
cgctgtagac accgttcctc atgctgccgg gtgggttttg cagaagctcc cttagtgatt      3000
tcatgtttaa caggcagcat ccattttcag aatttcctgg cattgattta tattttgaag      3060
catacaggaa acttctcgtt tcctcgttta gccccaccca gatcaggtga aagggcagct      3120
ttaatggtgg tttttatgga ccacattatc agagagcact gtgcaagcca aatggttcaa      3180
taatgaatga aaattctggg tgtaaagagt aaatatgccc tggctctttc taccaatgtt      3240
tgctcctggt tggaaagaaa ccaaagattt aagacgggct gctcttccag actggctgtg      3300
cctgcctgtg cccagcaacc tgtgcagccg gcagtgtgcc tggtgtcacg ccaggaggct      3360
gtggctgctg tgggccctct ggaattgtgc tcctcacaaa gtttccccaa aaggttcttc      3420
taagccttta ttgtccctgg taaatgtttc ccggctgggc gcggtggctc acgcctgtaa      3480
tcccagcact ttgggaggcc gaggcgggtg gatcacctaa ggtcaggagt ttgagatcag      3540
cctgcccaac atggtgaaac ctcgtctcta ctaaaaatac acaacttagc cagtcttgtt      3600
ggcgcacgcc tgtaatctca gctactaggg acgctgaggc aggagaatcg cttgaaccca      3660
agaaagaggt ggaggttgcg gtgagccaag attgcgccac tgcactccag cctgggcaaa      3720
cagagggaga ctccatcgcc cccccccaac aaaaaaaaaa gtttcccata cactggcctg      3780
ccccaaaacc cactaacaat tttagcaaaa cagtccaggc caaagaggaa gcatttcatg      3840
ttcaataaga aacccagcca ttccgcatgg ctggttcctg agtggctctg gtgatactct      3900
ccagccacct gctgacattg agaatctcag acctcgggac tgctgttgcg gtaccgtgtg      3960
tctgacacct gccagcagcc ctttgctatc tgcgcgcagg atggggggtga ctgcccagac      4020
```

- 11 -

```
attcccgcta gataggctct gatttccggg gcagcctttc agatgcggca gacatacaac        4080
acctgtactt tagagtttta agggaaaaaa aatcagaagt gctggttaga tagtaaaaac        4140
ttaggataac ttagaaaggc tagttttagc ttcctttgtg gctccctggt gcaaaacaat        4200
tagcagttat gcaatggacc tgattctagt ttattctaat taagaagtga ggccgagttt        4260
gacttcgttc ctgaatacaa tcttgagtaa ctgggaaagt ctgagtgaaa ggatggcctc        4320
attctctttc taatcttgct ggtttcaaga ttagaaaatg gcattatttg atctgaaatg        4380
tttgagaaga cacgaataaa gttacttggg cag                                     4413
```

- 12 -

FIG. 1

```
Q: 1      PKHLLVFINPFGGKGQGKRIYERKVAPLFTLASITTDIIGNKFYVNYVEVITEHANQAKE
          P..LL:.:NPFGG:G . : :..V.P:.: A.:: ::I TE..N.A:E
H: 144    PPRLLLLVNPFGGRGLAWQWCKNHVLPMISEAGLSFNLIQ----------TERQNHARE


          TLYEINIDKYDGIVCVGGDGMFSEVLHGLIGRTQRSAGVDQNHPRAVLVPSSLRIGIIPA
           .:. :::.::DGIV.V.GDG:..EVL:GL:.R .: ..AV :P :GI:P.
          LVQGLSLSEWDGIVTVSGDGLLHEVLNGLLDR-------PDWEEAVKMP----VGILPC


          GSTDCVCYS---------TVGTSDAETSALHIVVGDSLAMDVSSVHHNSTLLRYSVSLLG
          GS :.:. : .:G.. . ..:L :. G.. .:D: SV S :S. :.
          GSGNALAGAVNQHGGFEPALGLDLLLNCSLLLCRGGGHPLDLLSVTLASGSRCFSFLSVA


          YGFYGDIIKDSEKKRWLGLARYDFSGLKTFLSHHCYEGTVSFLPAQHTVGSP 223
          :GF..D: .SE: R LG AR:... : ..: H.Y.G.:S:LPA. . .SP
          WGFVSDVDIQSERFRALGSARFTLGTVLGLATLHTYRGRLSYLPATVEPASP 352
```

FIG. 2

PKHLLVFINP FGGKGQGKRI YERKVAPLFT LASITTDIIG NKFYVNYVEV ITEHANQAKE TLYEINIDKY

DGIVCVGGDG MFSEVLHGLI GRTQRSAGVD QNHPRAVLVP SSLRIGIIPA GSTDCVCYST VGTSDAETSA

LHIVVGDSLA MDVSSVHHNS TLLRYSVSLL GYGFYGDIIK DSEKKRWLGL ARYDFSGLKT FLSHHCYEGT

VSFLPAQHTV GSPRDRKPCR AGCFVCRQSK QQLEEEQKKA LYGLEAAEDV EEWQVVCGKF LAINATNMSC

ACRRSPRGLS PAAHLGDGSS DLILIRKCSR FNFLRFLIRH TNQQDQ